



RECEIVED

JUN 05 2001

TECH CENTER 1600/2900

1

SEQUENCE LISTING

<110> HONORE, ERIC
FINK, MICHEL
LAZDUNSKI, MICHEL
LESAGE, FLORIAN
DUPRAT, FABRICE

<120> MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
OF SAID CHANNELS IN DRUG SCREENING

<130> 1383-00

<140> 09/655,272

<141> 2000-09-05

<150> PCT/FR99/00404

<151> 1999-02-23

<150> FR 98/02725

<151> 1998-03-05

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 1757

<212> DNA

<213> Unknown Sequence

<220>

<221> CDS

<222> (284)..(1477)

<220>

<223> Description of Unknown Sequence: DNA encoding TRAAK

<400> 1

ccacgcgtcc gcggacgcgt gggtcgccca cgcgtccggt ggcggctgtc ctgagccccc 60
ggccagctga tgtccaggtt agggcagcgt tggggcccca atcccagcct ggaaggttgg 120
acttcacgtc gacccttctc tgagtcttct gccactcact ggcctggaca agacagcatt 180
ggggagccca gaggctgcag gtgcagtgac cactgctccc caggagctcc ctgctccttc 240
ttcccaggca ggaagtggag ctggacctgc ctctggaagg acc atg cgc agc acc 295
Met Arg Ser Thr

1

aca ctc ctg gct ctg ctg gca ctg gtg ctg ctt tac ttg gta tct ggg 343
Thr Leu Leu Ala Leu Leu Ala Leu Val Leu Leu Tyr Leu Val Ser Gly
5 10 15 20

gct cta gtg ttc cag gct ctg gag cag cct cac gag cag cag gct cag 391
 Ala Leu Val Phe Gln Ala Leu Glu Gln Pro His Glu Gln Gln Ala Gln
 25 30 35

aag aaa atg gat cat ggc cga gac cag ttt ctg agg gac cat ccc tgt 439
 Lys Lys Met Asp His Gly Arg Asp Gln Phe Leu Arg Asp His Pro Cys
 40 45 50

gtg agc cag aag agc ctg gag gat ttc atc aag ctc ctg gtt gaa gcc 487
 Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu Leu Val Glu Ala
 55 60 65

ctg gga ggg ggc gca aac cca gaa acc agc tgg acc aat agc agc aac 535
 Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr Asn Ser Ser Asn
 70 75 80

cac tca tca gct tgg aac ctg ggc agc gcc ttc ttt ttc tcg ggg acc 583
 His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe Phe Ser Gly Thr
 85 90 95 100

atc atc act acc atc ggc tat ggc aat ata gtc tta cac aca gat gcc 631
 Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu His Thr Asp Ala
 105 110 115

ggg cgt ctc ttt tgt atc ttc tat gca ctg gtg ggg atc cca ctg ttc 679
 Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly Ile Pro Leu Phe
 120 125 130

ggg atg ctg ctg gcg gga gtc ggg gac cgg ctg ggc tcc tct ctg cgc 727
 Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly Ser Ser Leu Arg
 135 140 145

cgg ggc atc ggc cac atc gaa gca atc ttc ttg aag tgg cat gtg cca 775
 Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys Trp His Val Pro
 150 155 160

ccg ggg ctg gtg aga agt ctg tcc gca gtg ctc ttc ctg ctg atc ggc 823
 Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe Leu Leu Ile Gly
 165 170 175 180

tgc ctg ctc ttt gtc ctc act cct acc ttc gtg ttc tcc tac atg gag 871
 Cys Leu Leu Phe Val Leu Thr Pro Thr Phe Val Phe Ser Tyr Met Glu
 185 190 195

agc tgg agc aag tta gaa gcc atc tac ttt gtt ata gtg act ctc acc 919
 Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile Val Thr Leu Thr
 200 205 210

act gta ggc ttt ggc gat tat gta ccc ggc gat ggc acc ggg cag aac 967
 Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly Thr Gly Gln Asn
 215 220 225

tct cca gcc tac cag ccg ctg gtg tgg ttc tgg atc ttg ttt ggc cta 1015
 Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile Leu Phe Gly Leu
 230 235 240

gcc tac ttc gcc tca gtg ctc acc acc atc ggc aac tgg ttg cga gca 1063
 Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn Trp Leu Arg Ala
 245 250 255 260

gtg tcc cgc cga act cgg gca gag atg ggt ggc cta acg gca cag gct 1111
 Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu Thr Ala Gln Ala
 265 270 275

gct agc tgg acc ggc aca gtg aca gcg cga gtg acc cag cga act ggg 1159
 Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr Gln Arg Thr Gly
 280 285 290

ccc agc gcc ccg ccg cca gag aag gag caa cca ctc ctg ccc tcc tct 1207
 Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu Leu Pro Ser Ser
 295 300 305

ttg ccg gca ccg cct gct gtt gtt gag cca gcc ggc agg ccc ggc tcc 1255
 Leu Pro Ala Pro Pro Ala Val Val Glu Pro Ala Gly Arg Pro Gly Ser
 310 315 320

cct gca ccc gca gag aag gtt gag act ccg tcc ccg ccc acg gcc tca 1303
 Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro Pro Thr Ala Ser
 325 330 335 340

gct ctg gat tac ccc agt gag aat ctg gcc ttc atc gac gag tcc tca 1351
 Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile Asp Glu Ser Ser
 345 350 355

gac acg cag agt gag cgt ggc tgt gcc ctg cct ccg gct cct ccg ggt 1399
 Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg Ala Pro Arg Gly
 360 365 370

cgc cgc cga ccc aac cca tcc aaa aag cct tcc aga ccc ccg ggt cct 1447
 Arg Arg Arg Pro Asn Pro Ser Lys Lys Pro Ser Arg Pro Arg Gly Pro
 375 380 385

ggg cga ctc cga gac aag gcc gtg ccg gtg taggggcagg atctctggac 1497
 Gly Arg Leu Arg Asp Lys Ala Val Pro Val
 390 395

ccggatccca cgccagggt ttcgctcttg ctgatgctca ggcatgcttg gcttatttga 1557

ccaaagagcc gtccctcttt tgtccacgt ggttgcaacc ctgacaggag tccagtgggt 1617

gccaaatgcc accgctcttc cctggctggt tcttcacatc caatcatttc caaagcccac 1677

catccaaggc tttctgcctc gctcccctgc cggttttgac cctcacacct cacaactgtg 1737

cctcaaaacc tgcaccaata 1757

<210> 2

<211> 398

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: TRAAK

<400> 2
 Met Arg Ser Thr Thr Leu Leu Ala Leu Leu Ala Leu Val Leu Leu Tyr
 1 5 10 15
 Leu Val Ser Gly Ala Leu Val Phe Gln Ala Leu Glu Gln Pro His Glu
 20 25 30
 Gln Gln Ala Gln Lys Lys Met Asp His Gly Arg Asp Gln Phe Leu Arg
 35 40 45
 Asp His Pro Cys Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu
 50 55 60
 Leu Val Glu Ala Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr
 65 70 75 80
 Asn Ser Ser Asn His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe
 85 90 95
 Phe Ser Gly Thr Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu
 100 105 110
 His Thr Asp Ala Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly
 115 120 125
 Ile Pro Leu Phe Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly
 130 135 140
 Ser Ser Leu Arg Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys
 145 150 155 160
 Trp His Val Pro Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe
 165 170 175
 Leu Leu Ile Gly Cys Leu Leu Phe Val Leu Thr Pro Thr Phe Val Phe
 180 185 190
 Ser Tyr Met Glu Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile
 195 200 205
 Val Thr Leu Thr Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly
 210 215 220
 Thr Gly Gln Asn Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile
 225 230 235 240
 Leu Phe Gly Leu Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn
 245 250 255
 Trp Leu Arg Ala Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu
 260 265 270
 Thr Ala Gln Ala Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr
 275 280 285
 Gln Arg Thr Gly Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu
 290 295 300

Leu Pro Ser Ser Leu Pro Ala Pro Pro Ala Val Val Glu Pro Ala Gly
305 310 315 320

Arg Pro Gly Ser Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro
325 330 335

Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile
340 345 350

Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg
355 360 365

Ala Pro Arg Gly Arg Arg Arg Pro Asn Pro Ser Lys Lys Pro Ser Arg
370 375 380

Pro Arg Gly Pro Gly Arg Leu Arg Asp Lys Ala Val Pro Val
385 390 395

<210> 3

<211> 336

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: TWIK

<400> 3

Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu Arg
1 5 10 15

His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
20 25 30

Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
35 40 45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
65 70 75 80

Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
85 90 95

Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
100 105 110

Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
115 120 125

Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
130 135 140

Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
145 150 155 160

Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
165 170 175

Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
180 185 190

Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
195 200 205

Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
210 215 220

Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
225 230 235 240

Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
245 250 255

Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
260 265 270

Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
275 280 285

Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
290 295 300

Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
305 310 315 320

Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
325 330 335

<210> 4

<211> 370

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: TREK

<400> 4

Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser
1 5 10 15

Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg
20 25 30

Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser
35 40 45

Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val
50 55 60

Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile
65 70 75 80

Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser
 85 90 95
 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
 100 105 110
 Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
 115 120 125
 Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
 130 135 140
 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
 145 150 155 160
 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
 165 170 175
 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
 180 185 190
 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
 195 200 205
 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
 210 215 220
 Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
 225 230 235 240
 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
 245 250 255
 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
 260 265 270
 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
 275 280 285
 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
 290 295 300
 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
 305 310 315 320
 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
 325 330 335
 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
 340 345 350
 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr
 355 360 365
 Cys Leu
 370

<210> 5
 <211> 394
 <212> PRT
 <213> Unknown Sequence

<220>
 <223> Description of Unknown Sequence: TASK

<400> 5
 Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe
 1 5 10 15
 Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu
 20 25 30
 Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu
 35 40 45
 Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
 50 55 60
 Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
 65 70 75 80
 Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95
 Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
 100 105 110
 Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
 115 120 125
 Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
 130 135 140
 Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val
 145 150 155 160
 Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala
 165 170 175
 Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr
 180 185 190
 Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu
 195 200 205
 Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser
 210 215 220
 Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
 225 230 235 240
 Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg
 245 250 255

Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly
 260 265 270
 Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr
 275 280 285
 Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu
 290 295 300
 His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys
 305 310 315 320
 Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser
 325 330 335
 Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly Arg
 340 345 350
 Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg
 355 360 365
 Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe
 370 375 380
 Arg Gly Leu Met Lys Arg Arg Ser Ser Val
 385 390